Attorney Docket No.: 12674-006001

WHAT IS CLAIMED IS:

1	1.	A set of nucleic acids comprising:
2		a first pair of primers, each containing an oligo-nucleotide selected from the
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and
4		a second pair of primers, each containing an oligo-nucleotide selected from the
5		hexon gene region of adenovirus,
6		wherein each oligo-nucleotide has 14-40 nucleotides in length.
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1	2.	The set of nucleic acids of claim 1, further comprising:
2		a third pair of primers, each containing an oligo-nucleotide specific for human
3		parainfluenza virus 1;
		a fourth pair of primers, each containing an oligo-nucleotide specific for human
5		parainfluenza virus 3;
61		a fifth pair of primers, each containing an oligo-nucleotide specific for respiratory
<u> </u>		syncytial virus;
8		a sixth pair of primers, each containing an oligo-nucleotide specific for influenza
9		virus A; or
10=		a seventh pair of primers, each containing an oligo-nucleotide specific for
١Ē		influenza virus B;
⊒ 12∐		or a combination thereof.
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1	3.	The set of nucleic acids of claim 2, wherein
2		the oligo-nucleotides in the third pair of primers are selected from the
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,
4		the oligo-nucleotides in the fourth pair of primers are selected from the
5		hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,
6		the oligo-nucleotides in the fifth pair of primers are selected from the non-
7		structural protein 2 gene region of respiratory syncytial virus,
8		the oligo-nucleotides in the sixth pair of primers are selected from the non-
9		structural protein gene region of influenza virus A, and

10		the oligo-nucleotides in the seventh pair of primers are selected from the
11		hemagglutinin-neuraminidase gene region of influenza virus B.
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1	4.	The set of nucleic acids of claim 1, wherein
2		the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5
3		and 7, or SEQ ID NOs:6 and 7; and
4		the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID
5		NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.
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1	5.	The set of nucleic acids of claim 4, further comprising:
2		a third pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1
3–≟		and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
4=		a fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8
5		and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;
6 <u>.</u>		a fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:12
		and 14, or SEQ ID NOs:13 and 15;
8		a sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:
		16 and 18, or SEQ ID NOs:17 and 19; or
10		a seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID
1亿		NO:20 and 22, or SEQ ID NOs:21 and 23,
11 12		or a combination thereof.
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1	6.	A set of nucleic acids comprising:
2		a first nucleic acid obtained from amplification of a respiratory syncytial virus
3		nucleic acid template with a first pair of primers, each containing an oligo-nucleotide
4		selected from the non-structural protein 2 gene region;
5		a second nucleic acid obtained from amplification of an influenza virus A nucleic
6		acid template with a second pair of primers, each containing an oligo-nucleotide selected
7		from the non-structural protein gene region; or

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a third nucleic acid obtained from amplification of an influenza virus B nucleic acid template with a third pair of primers, each containing an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region,

or a combination thereof,
wherein each oligo-nucleotide has 14-40 nucleotides in length.

7. The set of nucleic acids of claim 6, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs: 16 and 18, or SEQ ID NOs:17 and 19; and

the oligo-nucleotides in the third pair of primers are, respectively, SEQ ID NOs:20 and 22, or SEQ ID NOs:21 and 23.

8. The set of nucleic acids of claim 7, further comprising:

a fourth nucleic acid obtained from amplification of a human parainfluenza virus 1 nucleic acid template with a fourth pair of primers, said fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fifth nucleic acid obtained from amplification of a human parainfluenza virus 2 nucleic acid template with a fifth pair of primers, said fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7;

a sixth nucleic acid obtained from amplification of a human parainfluenza virus 3 nucleic acid template with a sixth pair of primers, said sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11; or

a seventh nucleic acid obtained from amplification of an adenovirus nucleic acid template with a seventh pair of primers, said seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27;

or a combination thereof.

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1	9.	A set of nucleic acids comprising:
2		a first nucleic acid containing a first oligo-nucleotide selected from the non-
3		structural protein 2 gene region of respiratory syncytial virus,
4		a second nucleic acid containing a second oligo-nucleotide selected from the non-
5		structural protein gene region of influenza virus A, or
6		a third nucleic acid containing a third oligo-nucleotide selected from the
7		hemagglutinin-neuraminidase gene region of influenza virus B,
8		or a combination thereof,
9		wherein each nucleic acid has 20-1,000 nucleotides in length.
	10.	The set of nucleic acids of claim 9, wherein each nucleic acid has 20-500 nucleotides in length.
第 平 m 2 m	11.	The set of nucleic acids of claim 10, wherein each nucleic acid has 20-50 nucleotides in length.
	12.	The set of nucleic acids of claim 9, wherein each oligo-nucleotide is selected from the group consisting of SEQ ID NOs:40-52 and sequences complementary thereto.
1	13.	The set of nucleic acids of claim 12, wherein each nucleic acid has 20-500 nucleotides in
2		length.
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1	14.	The set of nucleic acids of claim 13, wherein each nucleic acid has 20-50 nucleotides in
2		length.
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1	15.	The set of nucleic acids of claim 12, further comprising a nucleic acid containing an
2		oligo-nucleotide selected from the group consisting of SEQ ID NOs:28-39, 53-57, and
3		sequences complementary thereto, wherein each nucleic acid has 20-1,000 nucleotides in

16.	The set of nucleic acids of claim 15, wherein each nucleic acid has 20-500 nucleotides in
	length.

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17. The set of nucleic acids of claim 16, wherein each nucleic acid has 20-50 nucleotides in length.

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18. A method of simultaneously detecting viruses which cause respiratory infections comprising:

providing a nucleic acid from a sample suspected of containing a virus to be detected;

amplifying the nucleic acid with a set of primers specific for a group of target viruses, said set of primers containing a first pair of primers, each having an oligonucleotide selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and a second pair of primers, each having an oligo-nucleotide selected from the hexon gene region of adenovirus, each oligo-nucleotide having 14-40 nucleotides in length; and

detecting amplification products; whereby detection of an amplification product specific for a target virus indicates the presence of the target virus.

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19. The method of claim 18, wherein, in the amplifying step, said set of primers further containing:

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a third pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 1,

a fourth pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 3,

a fifth pair of primers, each including an oligo-nucleotide specific for respiratory syncytial virus,

a sixth pair of primers, each including an oligo-nucleotide specific for influenza virus A, or

11		a seventh pair of primers, each including an oligo-nucleotide specific for
12		influenza virus B,
13		or a combination thereof.
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1	20.	The method of claim 19, wherein
2		the oligo-nucleotides in the third pair of primers are selected from the
3		hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,
4		the oligo-nucleotides in the fourth pair of primers are selected from the
5		hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,
6		the oligo-nucleotides in the fifth pair of primers are selected from the non-
7		structural protein 2 gene region of respiratory syncytial virus,
8_		the oligo-nucleotides in the sixth pair of primers are selected from the non-
9=		structural protein gene region of influenza virus A, and
1011		the oligo-nucleotides in the seventh pair of primers are selected from the
		hemagglutinin-neuraminidase gene region of influenza virus B.
1	21.	The method of claim 18, wherein
2-		the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5
3		and 7, or SEQ ID NOs:6 and 7; and
4 <u>1</u>		the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID
5		NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.
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1	22.	The method of claim 21, wherein said set of primers further containing:
2		a third pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:1
3		and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;
4		a fourth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:8
5		and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;
6		a fifth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:12
7		and 14, or SEQ ID NOs:13 and 15;
8		a sixth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs: 16
9		and 18, or SEQ ID NOs:17 and 19; or

10		a seventh pair of primers including, respectively, oligo-nucleotides SEQ ID
11		NO:20 and 22, or SEQ ID NOs:21 and 23;
12		or a combination thereof.
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1	23.	The method of claim 18, wherein the detecting step includes hybridizing the
2		amplification product to a set of probes, said set of probes containing:
3		a first probe having a first nucleic acid selected from the hemagglutinin-
4		neuraminidase gene region of human parainfluenza virus 2, and
5		a second probe having a second nucleic acid selected from the hexon gene region
6		of adenovirus,
7		each probe having 20-2000 nucleotides in length.
	24.	The method of claim 23, wherein each nucleic acid is selected from the group consisting of SEQ ID NOs:34-36 and 53-57.
	25.	The method of claim 19, wherein the detecting step includes hybridizing the
2		amplification product to a set of primers, said set of probes contains:
<u> </u>		a first probe having a first nucleic acid selected from the hemagglutinin-
₩ 4 <u></u>		neuraminidase gene region of human parainfluenza virus 2, and
2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		a second probe having a second nucleic acid selected from the hexon gene region
6		of adenovirus;
7		said set of probes further contains:
8		a third probe having a third nucleic acid specific for human parainfluenza virus 1,
9		a fourth probe having a fourth nucleic acid specific for human parainfluenza virus
10		3,
11		a fifth probe having a fifth nucleic acid specific for respiratory syncytial virus,
12		a sixth probe having a sixth nucleic acid specific for influenza virus A, or
13		a seventh probe having a seventh nucleic acid specific for influenza virus B,
14		or a combination thereof;
15		each probe having 20-2000 nucleotides in length.

- 1 26. The method of claim 25, wherein each probe is selected from the group consisting of
- 2 SEQ ID NOs:28-57.